

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 15:54:59 Search time 1605.5 Seconds  
(without alignments)  
7599.656 Million cell updates/sec

Title: US-09-733-507-1  
Perfect score: 904  
Sequence: 1 atctctctctcacagaga.....tatgttttggtactgata 904

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

ESN:\*  
1: em\_estha:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estimu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrtt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293.8	32.5	352	10 T88456	T88456 12152 Lambda
2	272	30.1	329	10 T21659	T21659 3667 Lambda
3	146.4	16.2	503	12 B78431	B78431 T27E12TF.1
4	102.2	11.3	1101	12 CNS0039C	AL063921 Drosophila
5	85.6	9.5	997	12 CNS005TE	AL060767 Drosophila
6	80.6	8.9	1101	12 CNS0182P	AL108811 Drosophila
7	77.8	8.6	987	12 CNS00418	AL106537 Drosophila
8	74.4	8.2	689	10 BM436399	BM436399 VVA003E05
9	68.6	7.6	1101	12 CNS0039C	AL063921 Drosophila
10	66	7.3	77	9 AM004548	AM004548 EST512225
11	65	7.2	585	10 BG643706	BG643706 EST511900
12	64.8	7.2	1101	12 CNS008MC	AL052719 Drosophila
13	64.6	7.1	928	12 CNS0102F	AL096433 Drosophila
14	63.6	7.0	1201	12 CNS0107R	AL096625 Drosophila
15	63.4	7.0	908	12 BH156237	BH156237 ENTREV74CF
16	63.2	7.0	1101	12 CNS000D1	AL065414 Drosophila
17	63	7.0	510	10 BH129591	BH129591 G092P90V

C 18	62.6	6.9	996	12 CNS00FVH	AL071053 Drosophila
C 19	62	6.9	987	12 CNS014PC	AL104456 Drosophila
C 20	61.8	6.8	1101	12 CNS0106X	AL098595 Drosophila
C 21	61.6	6.8	938	12 CNS006T3	AL065906 Drosophila
C 22	61	6.7	1125	9 AL547503	AL547503 AL547503
C 23	60.8	6.7	914	12 CNS002ZY	AL097768 Drosophila
C 24	60.6	6.7	623	10 BE347049	BE347049 sp34c09.Y
C 25	60.4	6.7	928	12 CNS00DKY	AL071885 Drosophila
C 26	60	6.6	617	12 A236172	A236172 RPC1-23-1
C 27	60	6.6	668	12 A2312109	A2312109 LM0027K13
C 28	59.6	6.6	1101	12 CNS0039R	AL063922 Drosophila
C 29	59.6	6.6	1101	12 CNS00EVL	AL069706 Drosophila
C 30	59.6	6.6	1101	12 CNS017KE	AL108152 Drosophila
C 31	59.2	6.5	1101	12 CNS0021T	AL061936 Drosophila
C 32	59	6.5	1001	12 CNS0155H	AL105023 Drosophila
C 33	58.8	6.5	846	12 CNS00KOV	AL078280 Drosophila
C 34	58.6	6.5	1101	12 CNS00FMC	AL070972 Drosophila
C 35	58.6	6.5	1204	12 CNS016E2	AL106658 Drosophila
C 36	58.4	6.5	896	12 CNS00BP8	AL035462 Drosophila
C 37	57.6	6.4	585	12 A2060400	A2060400 RPC1-23-4
C 38	57.6	6.4	1030	12 CNS02LP3	AL203088 Tetradon
C 39	57.4	6.3	777	12 CNS025WB	AL182612 Tetradon
C 40	57.2	6.3	821	12 CNS03P7F	AL241332 Tetradon
C 41	57.2	6.3	1101	12 CNS00P86	AL070280 Drosophila
C 42	57.2	6.3	1101	12 CNS017AS	AL108706 Drosophila
C 43	57	6.3	620	10 BE823380	BE823380 GM700019B
C 44	57	6.3	1101	12 CNS0100X	AL098379 Drosophila
C 45	56.4	6.2	424	10 B1503896	B1503896 BH170025A

## ALIGNMENTS

RESULT 1  
LOCUS T88456  
DEFINITION 12152 Lambda-PRL2 Arabidopsis thaliana cDNA clone 156J24T7, mRNA  
ACCESSION T88456  
VERSION T88456.1 GI:936292  
KEYWORDS EST.  
SOURCE T88456  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops.  
1 (bases 1 to 352)  
Newman,T., debruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh  
,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M., Retzel  
,E. and Somerville,C.  
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
Plant Physiol. 106, 1241-1255 (1994)  
95148729  
On Apr 14, 1993 this sequence version replaced gi:716808.  
Contact: Thomas Newman  
MSU-DOE Plant Research Laboratory  
Michigan State University  
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.  
Lansing MI  
Tel: 517-353-0854  
Fax: 517-353-9168  
Email: 22313tnc@dm.ci.msu.edu  
Seq primer: 17 dye primer.  
Location/Qualifiers  
1..352  
/organism="Arabidopsis thaliana"  
/strain="var columbia"  
/db\_xref="taxon:3702"  
/clone="156J24T7"  
/clone\_lib="Lambda-PRL2"  
/note="Vector: lambda Z1P-Lox; Site\_1: Sal; Site\_2: Not;  
Lambda PRL2 is a cDNA library derived from equal

## FEATURES

source

quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's lambda zip-lox. The cDNA inserts were directionally cloned with Sal-I Not arms using oligo dr primed cDNA. "

Query Match	32.5%	Score 293.8;	DB 10;	Length 352;
Best Local Similarity	88.3%;	Pred. No. 9.1e-38;		
Matches 310; Conservative	0;	Mismatches 41;	Indels 0;	Gaps 0;

[illegible]

Qy 76 gctcaagcaaatcttagaagctgtagtcttcgtcaacgtatatgcagctacgagccggaga 135  
|||||  
Db 61 ncttaaggcaattntagaagctggagttcgttcacgatatncaagcttacggagccggaga 120

QY 136 atgttctatgttgatcggaataacaaagctcgtctcgtgcgtagataatgagctt 195  
| | | | | | | | | | | | | | | | | | | | | |  
Db 121 attgctttntnngatcggaataatcaaacgtctgctccgctcgctgatatgatgagctt 180

QY 196 tcgtcgtcttctgctggaagcaatgaataagaagaagaaatcaatactctgagagag 255  
 |||||  
 Db 181 TCCTCGCTTGTGTGCGAAGCATTGANTTAAGANGAAGANTTAATACATCTGGAGGAG 240

Oy           gaagataaaagtctgtgacacttgaaacgcgcagcattatcgccagggcagaagaaggacctt         315  
| | | | |  
Db      241 GAGCATAAAGATGCGTGAACCTGAACAAGTCGCACGTATGCCGGGGGTACCAGAGAGAAGCTT   300

Uy    310 CCGGAAATCTGGAGGAGGAGGAAGAAGAACTTAAGTAAATCATCAGGAG    366  
      |||    |||    |    |    |    |    |    |    |  
 Db    301 TTNNNAATCTTGNGNNGAGGAGGTGAANGAGCTTTACTAATCCCTTGGG    351

RESULT	2			
T21659				
LOCUS	T21659	329 bp	mRNA	linear
				EST 07-JAN-1996

COLLECTION	0007	EMBLDB	FILE	RIADUPO05	CHIAI004	CDNA	CLONE	3002377	INRA
ACCESSION	sequence.								
VERSION	T21659								
	T21659.1	GI:	2757169						

thale cress.  
SOURCE  
Arabidopsis thaliana  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS

Rosidae; eurousids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 329)  
Newman, T., debruin, F. J., Green, P., Keegstra, K., Kende, H., McIntosh

**TITLE** Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones

**MEDLINE** 95148729  
On Jan 7, 1998 this sequence version replaced g1:914567.  
**COMMENT** Contact: Thomas Newman  
Non-Con. Nat. Research Institute

Michigan State University  
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.  
Lansing, MI  
tel.: 517-353-0954

FEATURES

Email: 22313tcn@lhm.cl.msu.edu

Seq primer: T7.

Location/Qualifiers

## FEATURES

Location/Qualifiers

**Source**

```

source
1. 329
/organism="Arabidopsis thaliana"
/strain="var Columbia"
/db_xref="taxon:3702"
/clone="96D15T7"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-lox. Site_1: Sal; Site_2: Not;
lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark - rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRL's lambda Zip-lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA. "
```

BASE COUNT	106 a	50 c	78 g	82 t	13 others
ORIGIN					

Query Match	30.18;	Score 272;	DB 10;	Length 329;
Best Local Similarity	94.78;	Pred. No. 2.9e-34;		
Matches 286;	Conservative 0;	Mismatches 15;	Indels 1;	Gaps 1;

```
QY      1 atctcctctccacaaagattgtaacttcacgcacacgtaacctaataatcgagaatgg-t 59
          ||||| |
Db       1 ATCTCTCTCTCACAGAGAATGTNACTTCACGCACACGTAACCTPAATCGAAGATGGT 60
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Dy 60 gagaaatatagaaaagctaaaggaaattgttagaagctcggaagtccgtaacgatatafca 119  
| | | | |  
Dd 61 GAGAAATATAGAAAACCTAAGAAGATTGTAGAACCTGGAGTTCGTTCAACGTAATNTNCA 120

Qy 120 gctacgagacgcgagaaattgcttatctgtatgcgaaatactagctctgtccocgctgt 179  
|||||  
Db 121 gctacgagacgcgagaaattgcttatctgtatgcgaaatactagctctgtccocgctgt 180

Qy 180 cgcgtaaatgagcttcgcgcgtccttgatggaaacgaataagaagaatt 239  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
Db 161 cgstgataatgcngttcatcgcttcttagtggagcaatgatntaaanncaagant 240

240 aaTaccacTcTg999gaagaaagaTaaagaTcggTgcacacTaaacTcgacTgTatcgac999t 259  
 |||||  
 Db 241 AATACATCTGGGGAGAGAGTTAAGATGCTGACACTGAACCTCGAGCTATCGNCGTT 300

Q7	300	9a	301
		1	
Db	301	NA	302

RESULT	3
B78431	
LOCUS	B78431
	503 bp
	DNA
	linear
	GSS 16-JAN-1990

sequence.  
ACCESSION B78431  
VERSION B78431.1 GI:2775070

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
1 (pages 1 to 503)  
Rounsley, S. D., Field, C. E., Bass, S., Linher, K., Linher, K., Golden, K.

J.C.  
TITLE  
A BAC End Sequence Database for Identifying Minimal Overlaps in  
Arabidopsis Genomic Sequencing. Update 3  
1997

Contact: Steve Rounsley  
Department of Eukaryotic Genomics  
The Institute for Genomic Research

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: rounslay@ligr.org  
Seq primer: M13-21  
Class: BAC ends  
High quality sequence stop: 503.

FEATURES  
source  
Location/Qualifiers  
1..503

/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="T27E12"  
/clone\_lib="TAMU"  
/sex="hermaphrodite"  
/note="Vector: BelosBAC11; Site\_1: HindIII; Site\_2: HindIII  
; Produced by Rod Wing"

BASE COUNT 163 a 122 c 77 g 140 t 1 others  
ORIGIN

Query Match 16.2%; Score 146.4; DB 12; Length 503;  
Best Local Similarity 98.7%; Pred. No. 3.5e-14;  
Matches 147; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atctctctctcaccgagattgttaacttcacgcacacgttaacttaactgaagatgtg 60  
Db 355 ATCTCTCTCTCACGAGATTGTGACTTCACGACACGTAACTCAAGATGCTG 414  
QY 61 agaaaatagaaaagcctaagaattgtagaagctgtagcttcgtcaacgtatagcag 120  
Db 415 AGAAATATAGAAAAGCTTAAGCAATTGTAGAGCTGAGTTGCTCAAGTATATGAG 474  
QY 121 ctacgagccggaggaattgtttatgttag 149  
Db 475 CTACGAGCGCGAGAAATTGTATGTTAG 503

RESULT 4  
CNS00396/C 1101 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #  
DEFINITION BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
AL063921  
AL063921.1 GI:4941778  
GSS.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

fruit fly.  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org/TheBDGP/Drosophila>  
melanogaster BAC library was prepared by Kazutoyo Osogawa and  
Aaron Mammosser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
Location/Qualifiers  
1..1101

/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCI-98"  
/clone="BACR08K10"  
/note="end : TET3"

BASE COUNT 201 a 64 c 131 g 202 t 503 others  
ORIGIN

Query Match 11.3%; Score 102.2; DB 12; Length 1101;  
Best Local Similarity 20.4%; Pred. No. 3.4e-07;  
Matches 167; Conservative 324; Mismatches 322; Indels 4; Gaps 2;

QY 78 taagaagattgtagaagctggaatttcgtcaacgtatagcgtacgagccgagaat 137  
Db 1100 KARRMGDDTWDRTKRDDMDWTWKWTKKDRADRNRAGDADRNRAMDAGCTWWTATW 1041  
QY 138 tgttatgttagatcgaaataatcaagctcgtccgtcgctcggtatagatgttc 197  
Db 1040 WWWWATWDTWMDKWWWWATAKTDTATWTTWRTAWRADWAGRDGAKRRDADADGA 981  
QY 198 gtctctctttagtggaagcaat-gaataagaagaagaattatcatcttggaagg 256  
Db 980 GRDGGRRKKRDKRDKDDDKGKKKKAARAKAKAKWMDMDKMDKMDKAKRKA 921  
QY 257 aagataaagatgtgtacacatcgaaacgtcgaatcgaggtgacgaagaaggactt 316  
Db 920 DDDGAGDDGDKKDDDDTDTGTRKDDDDKMDMDKAGTGDTWMAAATDWWWWG 861  
QY 317 tgaaatctggaagaagagagagaagaagattaaagaaatcgaatattatcat 376  
Db 860 WADADWTTDAADADWADDRMDARWAKWDMAMGANTADRDMDGRAGKRGAKRRD 801  
QY 377 cgaatttgatcggcgggttaaagaatcgttagattgttgttagcggaggaagaa 436  
Db 800 RKRADDKRDADDDADDAATWTTTTRTDMDWMTDTWMAADRTMDDDDD-- 741  
QY 437 tggagagagacggtgacgagcgagagagagagagagagcaaatitagaagagatgcaa 496  
Db 742 -DAGTAGGKKMRTRRRKRRTDTRWDADADTRDRDRRRGDDAGGKTKRKR 664  
QY 497 cgaatcgaagaattgaagaattttttgtggaagctggaagaacaactgaagaataatca 556  
Db 683 RDRBATWDRTDAMWADAAMWTTTDTGTDWDRKDRKRKGARRRTTARAAWMDWTKAW 624  
QY 557 agaagaagatcaattcgatttcgagaagaagacatagaagaagcgttaagaatggg 616  
Db 623 DWAKMDWKTADRWMDRMAADTWDARADRWAKARARARARARARARARWTTTGKT 564  
QY 617 taaagttagagtggaagaagaagaagattatggtttttttttaaactttatgattt 676  
Db 563 TTAATWTTMAARAAMWMAATTTATWTTTWTWTTTWTWTTTWTWTTTAAWMAWMT 504  
QY 677 aatatcgaagaataagttatattatcttggtgatttggaaatataagaattgttga 736  
Db 503 ATWAAATTAAMWAAAAAATAATTTTWTWMTAAWMTAAWMTWTTTWTWMAA 444  
QY 737 ggaatgtttttagaagaatcgacagaagaagaagaagaagaagcttttaacagattt 796  
Db 443 TTTTWTWTTWMAATTAATTTTWTWTTWTTWTTWTTWTTWTTATATKCCCCCCTT 384  
QY 797 agagccagagaagaatgctgctttagcttaacttaactctctcttcgaactgtgtga 856  
Db 383 CCACCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 324  
QY 857 tctttagacatctcttagttagcattttagattt 893  
Db 323 YYYCYYYCYCCYTCNCNCYYYCYCTTTCYTYTTT 287

RESULT 5



```

QY 206 gtagtgagcaatgataataagaagaataatacatctgagaggaataaag 265
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 545 GMEKAKGAAGGGRGGRBVGNGRDATATATAAADAADTKRMBDARGAAGAAADAAA 604
QY 266 atggtcaacctaacaactgcacgtatcgaggggtcagaagaagaagcttttgaatc 325
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 605 RMAAKTWTMAAARAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 664
QY 326 tgaagaagaagaagaagaagaataaagtaataatccatgagaatattcatcggaattg 385
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 665 GGAATAADARRGGRGRRRRAAARAAAADAKAAAAAATAAATAAATAAATAAATAA 724
QY 386 aatcgaggttaagaatcgttagattgtgtgagcggaggaagaagaatgagaga 445
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 725 GGCXDCGKATKTAAMAKGKMGFTATAMWTWATWADTWAKATDADAKRAAGRRKRDAR 784
QY 446 cgtgagcggcggagagagagaggaatgagcgaattgagcggagtgccacggaacgcg 505
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 785 KTRADGGRARRRRRAAAGKRAAGARRAARAAADDDMDMAAATAAATAAATAAATAA 844
QY 506 aaattgaagatttt-ttgtgaagctgagaacaactcaagaataatcaagaagaag 564
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 845 TTRDRBWWMDMDWDTFMDDDTTAAWWDABARABRRRRRRRRRAAARAAADDDTDK 904
QY 565 tacaatttcgatttcgagaagaagaagccatagaagaagcttaagatgggttaagttta 624
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 905 DRWADATTKDPTTKTTTDDDDWDAKRRWMAAADAAMWRDARDAWMAATAKDDDGW 964
QY 625 gaagtagagaagaagaagaagttatgatttttttttttttttttttttttttttttt 684
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 965 KDWGGRGRKRGGRKRWKRGKTKGKDDDDWDXKTRDMMWMTTKKDDMMWDDGRRGR 1024
QY 685 aaggaaataagtaattttttttgtgatttggaataatgaatttgaagaagaagtt 744
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 1025 WTKRRKGAWMARADBDTDGKDTADKRRKTDTKRGDDWRKDRKRRDKGCD 1084
QY 745 ttgaagaagtaagaatt 761
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 1085 DKTKKDATWDDDDARDW 1101
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |

RESULT 7
CNS00418/c 987 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence Tm3 end of BAC #
DEFINITION BACR09C16 of RPCI-98 library from Drosophila melanogaster (fruit
fly) genomic survey sequence.
ACCESSION CNS00418
VERSION AL066537
KEYWORDS AL066537.1 GI:4942778
SOURCE GSS.
ORGANISM fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscocomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 987)
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Osegaawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library

```

```

FEATURES
    source
        /organism="Drosophila melanogaster"
        /db_xref="taxon:7227"
        /clone_1id="RPCI-98"
        /clone="BACR09C16"
        /note="end : Tm3"
BASE COUNT 238 a 162 c 17 g 177 t 393 others
ORIGIN
Query Match 8.6%; Score 77.8; DB 12; Length 987;
Best Local Similarity 25.6%; Pred. No. 0.0029;
Matches 112; Conservative 134; Mismatches 191; Indels 0; Gaps 0;

QY 208 agtgaagaatgataataagaagaataatacatctgagaggaagaataaag 267
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 916 ARARAAARAAARAAARAAARAAARAAARAAARAAARAAARAAARAAARAAAR 857
QY 268 gttgacactgaagctgcacgtatcgagcgggtgcagaagaagcttttgaatctg 327
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 856 RRRGGRGAGGRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 797
QY 328 agagaagagagagaagaagaatgaataatccatgagaaattatcggaaattgaa 387
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 796 RGRGRRGAGGAGGGAARARARARARARARARARARARARARARARARARAA 737
QY 388 tggcggttaagaatcgttagattgtgtgtgtgagcggaggaagaagatgagaagc 447
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 736 AARAAAGARAAARAAARARARARARARARARARARARARARARARARARAR 677
QY 448 gtgagcggagagagagagagagcgaattgatacgagagatccacaggaatcgaa 507
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 676 RGARRRRGAGRRRRRGARRRGARRGARRGARRGARRGARRRARRRARRAGARGA 617
QY 508 atggaagattttttgtgaaagctgagaacaactccaagaataatcaagaagaatc 567
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 616 RRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 557
QY 568 aatttcgatttcgagaagaagaagccatagaagaagcttaagatggtgataagttag 627
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 556 GGRGRRRRGRRGRRGGGGGRRGRRGRRGRRRRRRRRRRRRRRRRRRRRRRRGA 497
QY 628 tgaagaagaagaagaag 644
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 496 RRAARAAAGAGAGARAG 480
| : : | | : : | | : : | | : : | | : : | | : : | | : : | |

RESULT 8
BMA36399
LOCUS BMA36399 689 bp mRNA linear EST 31-JAN-2002
DEFINITION VVA003E05.52381 An expressed sequence tag database for abiotic
stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera
CDNA clone VVA003E05.5, mRNA sequence.
ACCESSION BMA36399
VERSION BMA36399.1 GI:18458121
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 689)
AUTHORS Cramer, G. R. and Cushman, J. C.
TITLE An expressed sequence tag database for abiotic stressed leaves of
JOURNAL Vitis vinifera var. Chardonnay
CONTACT: Cushman JC
UNPUBLISHED (2002)
JOURNAL Department of Biochemistry
COMMENT University of Nevada

```



Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,  
Gongone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,  
Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,  
Pollock, J., Suzuki, G., Argentine, C., Shah, S., Nobrega, A., Murry, L.,  
Turner, C., Kikoria, S., Elder, L., and Hanson, D.  
Arabidopsis thaliana Gene Expression Microarray  
Unpublished (1999)  
Contact: David Smoller, Ph.D.  
Genome Systems, Inc., a wholly owned subsidiary of Incyte  
Pharmaceuticals, Inc.  
4633 World Parkway Circle, St. Louis, MO 63134, USA  
Tel: 877-577-2733  
Fax: 314-427-3324  
Email: service@genomesystems.com.

## FEATURES

source  
Location/Qualifiers  
1..77  
/organism="Arabidopsis thaliana"  
/db\_xref="taxon:3702"  
/clone="70193225"  
/clone\_lib="A. thaliana, mixed source"  
/note="This sequence was obtained from a clone generated  
with a PCR product of the target gene."  
BASE COUNT 17 a 19 c 12 g 29 t  
ORIGIN

Query Match 7.3%; Score 66; DB 9; Length 77;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 gtacgaattgcacagaaagaaagacgttttaacagatttagagccacagaagt 811  
|||||  
Db 66 gthcgaattgcacagaaagaaagacgttttaacagatttagagccacagaagt 7

QY 812 cgtgtc 817  
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Db 6 cgtgtc 1

RESULT 11  
Bg643706 585 bp mRNA linear EST 24-APR-2001  
LOCUS EST511900 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
DEFINITION CTOF32G10 5' sequence, mRNA sequence.  
ACCESSION Bg643706  
VERSION Bg643706.1 GI:13778931  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.

REFERENCE 1 (bases 1 to 585)  
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Uterback, T.,  
Hansen, C., Rohnig, C. and Tanksley, S.  
Generation of ESTs from tomato shoot/meristem tissue  
Unpublished (2001)  
CONTACT: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.

## FEATURES

source  
Location/Qualifiers  
1..585  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="CTOF32G10"  
/clone\_lib="tomato shoot/meristem"  
/tissue\_type="shoot/meristem"  
/dev\_stage="developing shoots from 4-6wks old plants"  
/lab\_host="SOLR"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Small expanding leaves from the growing tip were  
taken from greenhouse plants (4-6wks old TA456). Tissue  
was immediately frozen in liquid nitrogen."  
BASE COUNT 193 a 108 c 144 g 140 t  
ORIGIN

Query Match 7.2%; Score 65; DB 10; Length 585;  
Best Local Similarity 67.2%; Pred. No. 0.37;  
Matches 92; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 490 atgccaaaggaatcggaaatgaatttttctggaagctgagaacaactcaagaa 549  
|||||  
Db 240 atcccaacagactctgaaatggaagagttttaccgcagaaaagacagacagaa 299  
QY 550 aaattcagaagaagtaaatctgatttcagaagaagaagccattagaagacttac 609  
|||||  
Db 300 aaattcagcagaagactgacactttgattccagtgaaagaccccttccggacgttac 359  
QY 610 gaatggtaaatgtaga 626  
|||||  
Db 360 gaatggcgaagatgaaa 376

RESULT 12  
CNS008WC/C 1101 bp DNA linear GSS 03-JUN-1999  
LOCUS CNS008WC  
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR18L14 of RPc1-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL052719  
VERSION AL052719.1 GI:4934268  
KEYWORDS fruit fly.  
SOURCE Drosophila melanogaster  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 1101)  
Direct Submission  
Genoscope.  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
Determination of this BAC end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Googawa and  
Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPc1-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source  
Location/Qualifiers  
1..1101  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPc1-98"  
/clone="BACR18L14"  
/note="end : TET3"  
BASE COUNT 145 a 171 c 122 g 340 t 323 others  
ORIGIN  
Query Match 7.2%; Score 64.8; DB 12; Length 1101;  
Best Local Similarity 31.5%; Pred. No. 0.34;

Matches 128; Conservative 102; Mismatches 165; Indels 11; Gaps 1;

```
OY      382 ttgaaatcgagcttaagaagtgcgtgaattcgttcttgtagagggaagaacgatgg          441
       ||| :||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      1001 TWTWTTTTRRACKTGDDADAAKTKWKAKDGTGTGGCGGCTGCAGWAATWGTRKKRGKG   942

OY      442 gaacgcgttcagcgcgaaggaaggaagcgaactlgtataccgaagtaccacgaa        501
       ||| :||::||::||::||::||::||::||::||::||::||::||::||::||
Db      941 RKDGGRGRRGCKGGGGCGMGCMGRKGMWRDTAAGDGGRKCMDFKACKDKCATGGGKCW    882

OY      502 tcggaattggaagtlltttlctgtgaagctcgagaaacaactcaagaaaattcaagaag    561
       ||| :||::||::||::||::||::||::||::||::||::||::||::||::||
Db      881 GTGTCAATTWTAATRWMTWARRTTWNRARRAMWMAWMWTTTTWTCATAATGAKMAMMMWK    822

OY      562 aaatacaatttcgacttcgagaagaagaagccaattgaaggaacgtlaagatlggtgaag     621
       ||| :||::||::||::||::||::||::||::||::||::||::||::||::||
Db      821 AAATTWMAATITWWTTATATITTAAACRAARAAMWTAAAWMATTAABAATTAAMWWWRRAPARTT 762

OY      622 ttagagtcgaagaagaagaagaagttatg-----gtttttttttaaccttla         670
       ||| :||::||::||::||::||::||::||::||::||::||::||::||::||
Db      761 TWAAAAARAAAAMDAAAIWTWTATDWTTTAAARAARAADAOKATTTTATATTATWTTWTT    702

OY      671 gatttaaatcatctcagggaaataagctaatttcatttgttgcgttggsaatalataaagtt     730
       ||| :||::||::||::||::||::||::||::||::||::||::||::||::||
Db      701 GTTTTTAAWPTGTGTTTDDRMRMKRRPRTTIGTTTRATATKTTHKKWAMWTTTATWTW      642 ,

OY      731 gtgcgaggaatcgttttcgaagctcgaatatcgaaatcgacgcgaaaaagaag          776
       ||| :||::||::||::||::||::||::||::||::||::||::||::||::||
Db      641 TRGGTGRRRDRATTGAATAAATAAAAAAAAAAANAANNTTAAANAAGC           596
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RESULT	13
CNS0102F/c	
LOCUS	
DEFINITION	CNS0102F 928 bp DNA linear GSS 26-Jul-1999
	Drosophila melanogaster genome survey sequence T7 end of BAC
	BACN03B09 of DrosBAC library from Drosophila melanogaster (fruit
	fly), genomic survey sequence.
ACCESSION	AL098433
VERSION	AL098433.1 GI:5610044
KEYWORDS	GSS.
SOURCE	fruit fly.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 928)  
Genoscope.  
Direct Submission  
Submitted (23-jul-1999) Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Allaud at CEPI (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBac11.

Matches	146,	Conservative	183;	Mismatches	247;	Indels	5;	Gaps	3;
QY	210	tggaaagcaatgaataaagaagaattatacatctgagaggaagataaagatg	269						
Db	926	wcgaataakagmmwmwgrmaatdpwatkwtkakrmwagrtmatkarkakagcaakrw	867						
QY	270	tgcactgaaagctgcagctatcgacgggtgacgaagaagaagcttttggaaacttgg	329						
Db	866	aaawataakkkwotrmgaktwradkkdvgctgtgwtwgrgkrkrrcgagagdgdtgrgr	807						
QY	330	agagagggagaagaagaattaaatccatgagaaattatcatcggaaattgaac	389						
Db	806	trrraagkagmkaakaratamaadwgrmamaaadaigagatmmwmatmtatataka	747						
QY	390	ggcgggttaaagaactgtagattgttgttctagcggagaaaacgaigagagacgt	449						
Db	746	tattaaawmrhndaraalctgkwrfgcttaagatkgwmdtra-dakkaagttatant	688						
QY	450	gacggggggaggaagagaagcttgaacggagatcccaaggaactcgaaat	509						
Db	687	atrtgtaakddarkakakmmwkatkakaagatatraamaatgadwagtwtgmkkttagaktgt	628						
QY	510	tgaagatttttctgtggaagctcgagaacaaactcaagaagaattcaagaagatcac	569						
Db	627	agmtgskmtddkwmrkrdkrdatgsmraatw---agaadawmrwgmaagtgaaerrwdgw	571						
QY	570	tttcgaattccagagaagagaaagccattgaaagacgcttcgaatggatagtagtg	629						
Db	570	rmfarsddrrkrkgaabrragaaaaagctgadadadrraargkkgdgkrrkgtkaaaag	511						
QY	630	aagaaagaagaagaagttaatgttttttctaacttttagattttaaatttcaggga	689						
Db	510	gmwagabradgdgrrgmwkkkkaadkktktwdtrtdkaakaktgaktgdgakraagdx-	450						
QY	690	ataagtaattatcttctgtgatttggaaataaagaattgttagagaagatttttag	749						
Db	451	rkxggagacatrttgcgwmwdwatttgawtmtatgtrtatatkaamakagawtrakraagrak	392						
QY	750	aagtaagaaattgcacagaaaaagaagaagacttttcaag	790						
Db	391	rraawgaaaaakgagakraakgraaalraannnnnnnnnnn	351						

REFERENCE	AUTHORS	JOURNAL	COMMENT
CNS0107R/c	LOCOS	DEFINITION	RESULT 14
CNS0107R	1201 bp	DNA	linear
Drosophila melanogaster genome survey sequence T7 end of BAC			GSS 26-JUL-1999
BACNO303g1 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
AL098625			
AL098625.1	GI:5610236		
GSS.			
fruit fly.			
Drosophila melanogaster			
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;			
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
1 (bases 1 to 1201)			
Genoscope.			
Direct Submission			
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :			
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
Determination of this BAC-end sequence was carried out as part of a			
collaboration with the European Drosophila Genome Project (EDGP) -			
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC			
library (Dros BAC) was made by Alain Billaud at CPHF (Centre			
d'Etude du Polymorphisme Humain) with funding provided by a MRC			
project grant. The DNA was prepared from embryos by Alain Bucheton			
and Genevieve Payan. It has been constructed in the vector			
pBeloBac11.			

FEATURES	Location/Qualifiers
source	1. .1201





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 15:54:59 ; Search time 47.3 Seconds  
(without alignments)  
4694.560 Million cell updates/sec

Title: US-09-733-507-1  
Perfect score: 904  
Sequence: 1 atctctctctcacagaga.....tatgtttgtgactgata 904

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 38353 segs, 122816752 residues  
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	92.6	10.2	7218	1 US-08-232-463-14	Sequence 14, Appl
2	47.8	5.3	289	4 US-09-007-005-17	Sequence 17, Appl
3	47.8	5.3	289	4 US-09-244-796-17	Sequence 17, Appl
4	43.6	4.8	16442	3 US-08-781-891-208	Sequence 208, App
5	42.8	4.7	19124	2 US-08-487-8268-13	Sequence 13, Appl
6	42.4	4.7	19124	2 US-08-487-8268-13	Sequence 13, Appl
7	42.4	4.6	4526	1 US-07-855-412B-4	Sequence 4, Appl
8	42.4	4.6	4526	2 US-08-308-887A-4	Sequence 4, Appl
9	42.4	4.6	4526	3 US-08-881-094-4	Sequence 4, Appl
10	41.8	4.6	7832	4 US-09-004-838-94	Sequence 94, Appl
11	41.4	4.6	1669	4 US-09-461-697-184	Sequence 184, App
12	41.2	4.6	5852	1 US-07-867-106-2	Sequence 2, Appl
13	41.2	4.5	1365	1 US-07-807-043B-4	Sequence 4, Appl
14	41.2	4.5	1365	1 US-08-299-849B-4	Sequence 4, Appl
15	41.2	4.5	1365	2 US-08-142-368A-4	Sequence 4, Appl
16	41.2	4.5	1365	3 US-08-967-727-4	Sequence 4, Appl
17	41.2	4.5	1365	4 US-08-037-230D-4	Sequence 4, Appl
18	40.8	4.5	1654	3 US-08-913-842-20	Sequence 20, Appl
19	40.8	4.5	1744	3 US-08-913-842-27	Sequence 27, Appl
20	40.8	4.5	1875	3 US-08-913-842-2	Sequence 2, Appl
21	40.8	4.5	1965	3 US-08-913-842-2	Sequence 2, Appl
22	40.4	4.5	1972	1 US-08-463-048-1	Sequence 1, Appl
23	40.4	4.5	1972	1 US-08-463-229-1	Sequence 1, Appl
24	40.4	4.5	1972	2 US-08-302-891-1	Sequence 1, Appl
25	40.4	4.5	51259	3 US-08-781-891-209	Sequence 209, App
26	39.8	4.4	10968	2 US-08-680-337-2	Sequence 2, Appl
27	39.8	4.4	10968	4 US-09-228-246-1	Sequence 1, Appl

## ALIGNMENTS

C 28	39.6	4.4	1117	4 US-09-247-3735-33	Sequence 33, Appl
29	39.4	4.4	2255	4 US-08-871-5728-3	Sequence 3, Appl
C 30	39.4	4.4	5506	4 US-09-004-838-93	Sequence 93, Appl
31	39.2	4.3	599	4 US-09-328-111-147	Sequence 147, App
32	39.2	4.3	1298	3 US-08-948-705-3	Sequence 3, Appl
33	39.2	4.3	273	2 US-08-737-298-1	Sequence 1, Appl
34	39.2	4.3	3211	2 US-08-574-959A-8	Sequence 8, Appl
35	39.2	4.3	3211	4 US-09-357-014-8	Sequence 8, Appl
36	39.2	4.3	3901	2 US-08-574-959A-6	Sequence 6, Appl
37	39.2	4.3	3901	4 US-09-357-014-6	Sequence 6, Appl
38	39.2	4.3	5852	1 US-07-867-106-2	Sequence 2, Appl
39	38.8	4.3	243	1 US-08-182-175A-56	Sequence 56, Appl
40	38.8	4.3	243	1 US-08-474-633A-74	Sequence 74, Appl
41	38.8	4.3	243	5 PCT-US92-06412-56	Sequence 56, Appl
42	38.8	4.3	1276	4 US-09-177-325-2	Sequence 2, Appl
43	38.8	4.3	1276	4 US-09-411-812A-2	Sequence 2, Appl
44	38.8	4.3	1276	4 US-09-590-113-2	Sequence 2, Appl
45	38.8	4.3	6243	2 US-09-056-075-1	Sequence 1, Appl

RESULT 1  
US-08-232-463-14/C  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHNEFLINGER, F.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)863-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: PT59pt-Fls  
US-08-232-463-14











QY 670 agatttaataatccagggaataagtttaatttattgttgatttggaataagatt 729  
|||||  
Db 5453 TTTTCTTAAATAATCAATAATTAATATCTATATATCTGATGAACTCAATTT 5394  
QY 730 tctaggaggaatgctttttagaagtcacgaattgcacgaaagaagaagcttttaac 789  
|||||  
Db 5393 TATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTCCA 5334  
QY 790 agattttaga 799  
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Db 5333 TCTTTTAA 5324

RESULT 13  
US-07-807-043B-4  
Sequence 4, Application US/07807043B  
Patent No. 5342774  
GENERAL INFORMATION:  
APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/807, 043B  
FILING DATE: 1991.1212  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,364  
FILING DATE: 23-SEPTEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838  
FILING DATE: 9-JULY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-MAY-1991  
TELECOMMUNICATION INFORMATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5342774man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LOD 253.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1365 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: singular  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
US-07-807-043B-4

Query Match 4.5%; Score 41; DB 1; Length 1365;  
Best Local Similarity 50.2%; Pred. NO. 0.48;  
Matches 101; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 510 tgaagattttgttgagctgagaaacaactcaagaagaattcaagaagttacaa 569  
|||||  
Db 1050 TGAAGAGCTTGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAAT 1109  
QY 570 ttccgatttcgagaagagagccatttagaagagctttagaatgggtcaagtttagtg 629

Db 1110 GGGAAACCCGATGCTTCACCTTAGCGATGCGAGTTGCAAGCCGACGAAGAAGAAAT 1169  
QY 630 aagaagaagaagattatgctttttttaaactttttagaatttaataattcagga 689  
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Db 1170 GGACAGCGGAG 1229  
QY 690 ataagtaatttattttttt 710  
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Db 1230 TCCAGAAATTTGATTGTGT 1250

RESULT 14  
US-08-299-849B-4  
Sequence 4, Application US/08299849B  
Patent No. 5612201  
GENERAL INFORMATION:  
APPLICANT: De plaen, Etienne; Boon-Falleur, Thierry;  
APPLICANT: Leith, Bernard; Szikora, Jean-Pierre; De Smet, Charles;  
APPLICANT: Chomez, Patrick  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In  
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/299, 849B  
FILING DATE: 1-SEPTEMBER-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,230  
FILING DATE: 26-MARCH-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/04354  
FILING DATE: 22-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/807,043  
FILING DATE: 12-DECEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,364  
FILING DATE: 23-SEPTEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838  
FILING DATE: 9-JULY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5612201man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LOD 5355  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1365 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
US-08-299-849B-4



Query Match	4.58;	Score 41;	DB 1;	Length 1365;
Best Local Similarity	50.2%;	Pred. No. 0.48;		
Matches 101; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

**QY** 510 tgaagatttttctgtgaaacctaagaacaactcaagaanaattccaaagaatcacaa 569  
|||||  
**Db** 1050 TGAAGAGCTTGCATGTGAAAGCAGACAGAAGAGAGAGAGAGAGAGAGAGAGAAAT 1108  
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**QY** 570 tttcgatltcgaagaagaagaagccattagaagaagcgtltaagaaatggtagagt 629  
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**Db** 1110 GGGAAACCCTGGATGGCTTCACACTTAGGCATGCATTGCCAAGCCCAAGAAAGAAAT 1168  
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**QY** 630 aagaagaagaagaagaagttacgcgttttttttaccttttgaaatttaattccaaggaa 689  
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**Db** 1170 GGACAGCGGAGAGAAGTGTTGTTTTTTTCCCCCTCATTAATTTCGTAGTTTATGAAA 1228  
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**QY** 690 ataagttcaatttatcttgtt 710  
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**Db** 1230 TCCAGAAATTTCATTTTGT 1250

RESULT 15  
US-08-142-368A-4  
; Sequence 4, Application US/08142368A  
; Patent No. 5925729  
; GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Boon-Fallure, Thierry; Van der Bruggen, Thierry; Elieenne-  
 APPLICANT: Van der Eynde, Benoît; Van Pel, Aline; De Plaen, Etienne-  
 APPLICANT: Lutquin, Christophe; Chomez, Patrick; Trevisari, Catia  
 TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
 TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
 NUMBER OF SEQUENCES: 26

ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM  
OPERATING SYSTEM: DD-DOS

OPERATING SYSTEM: PC-DOS  
SOFTWARE: wordperfect  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/142,368A  
FILING DATE: 02-MAY-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/04354  
FILING DATE: 23-MAY-1992

FILING DATE: 22 MAR 1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/807,043

FILING DATE: 12-DECEMBER-1991  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/764,364  
FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838

APPLICATION NUMBER: 9-JULY-1998  
PRIOR APPLICATION DATA: 07/005 500

APPLICATION NUMBER: 01/105,102  
FILING DATE: 23-May-1991  
INVENTOR/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5925729man D  
REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5253.4-US  
TELECOMMUNICATION INFORMATION:

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-142-368A-4

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Query Match	4.58;	Score 41;	DB 2;	Length 1365;
Best Local Similarity	50.28;	Pred. No. 0.48;		
Matches 101; conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

QY	510	tggagatttttctgtagaaccttagaacacatccaaagaataatccaagaagtaca	569
Db	1050	TGAAGAGCTTGCAATGGAAGAAGACACACAGACAGAGAGAGAGAGAGAGAAAT	1109
QY	570	tttcgatctcgagaagaagagaccattagaagagcttacgaatggtataagttagatg	629
Db	1110	GCGAACCOCGGATMGCTTTCACCTTAGGCATTCACATTCCAAAGCCCCAACAAAGAAAT	1169
QY	630	aagaagaagaagaagttaatvggtttttttttaaccttttagaatttaatatccaagg	689
Db	1170	GGACAGCGGGAAGAGGTGTTGTTTTTTTCCCTTCATTAATTTCTAGTTTATGATA	1229
QY	690	ataagttcaatttaatttgct	710
Db	1230	TCCAGAAAATTTCATTTTGTT	1250

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Search completed: September 4, 2002, 17:23:35
Job time: 5316 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: September 4, 2002, 17:23:40 (Search time 198.84 Seconds  
(without alignments)  
7805.726 Million cell updates/sec)

Title: US-09-733-507-1  
Perfect score: 904

Sequence: 1 atctctctctcaccagaga.....tatgttttgtagactgata 904

Scoring table: IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_032802:\*

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- 19: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	900.8	99.6	904	21	AA229415
2	774.8	85.7	779	21	AAC47352
3	757.8	83.8	780	21	AAC36958
4	72.4	8.0	804	21	AA229420
5	71.6	7.9	470	21	AA229403
6	71.6	7.9	470	21	AA95289
7	63.8	7.1	1341	21	AAC33295
8	63	7.0	620	21	AA202401
9	63	7.0	620	21	AAA95287

10	61.2	6.8	642	21	AA229418	Arabidopsis thaliana
11	60.6	6.7	16509	24	ABL33321	Human immune syste
12	60.4	6.7	870	21	AA25293	Arabidopsis thaliana
13	60.4	6.7	870	21	AAC6445	Arabidopsis thaliana
14	59.4	6.6	69	20	AA25038	Cyclin-dependent k
15	58.8	6.5	13125	24	ABL33226	Human immune syste
16	58.8	6.5	13125	24	ABL33226	Human immune syste
17	58.2	6.4	621	23	AA590688	Human metastasis a
18	58.2	6.4	4590	7	AA260472	DNA encoding novel
19	58	6.4	467	21	AA25291	Sequence encoding
20	57.6	6.4	533	21	AA229419	Soybean cyclin-dep
21	57.6	6.4	875	20	AA25016	Arabidopsis thaliana
22	57	6.3	1116	21	AA202402	Arabidopsis cyclin
23	57	6.3	1116	21	AA25288	Cyclin dependent k
24	56.4	6.2	1215	23	AA592075	Soybean cyclin-dep
25	55.4	6.1	61020	22	AA546788	DNA encoding novel
26	55	6.1	17848	22	AA545323	Tumour suppressor
27	54	6.0	1218	23	AA590730	Chemically pretrea
28	53.8	6.0	6650	24	ABL32639	DNA encoding novel
29	53.6	5.9	693	23	AA574240	Human immune syste
30	53.6	5.9	693	23	AA590715	DNA encoding novel
31	53.6	5.9	1839	22	AAH17145	DNA encoding novel
32	53.4	5.9	379	23	AA575428	Human cdna sequenc
33	53.4	5.9	379	23	AA590909	DNA encoding novel
34	53.4	5.9	14798	24	ABL33033	Human immune syste
35	53.4	5.9	15872	22	AA546519	Human immune syste
36	52.8	5.8	5822	24	ABL33096	Tumour suppressor
37	52.6	5.8	1193	20	AA255017	Human immune syste
38	52.6	5.8	6285	24	ABL33497	Alfalfa cyclin-dep
39	52.2	5.8	886	21	AAC37798	Human immune syste
40	52.2	5.8	932	20	AA255015	Arabidopsis thaliana
41	52.2	5.8	4415	24	ABL33906	Human immune syste
42	52.2	5.8	4415	24	ABL34602	Human immune syste
43	52.2	5.8	8456	24	ABL33976	Human immune syste
44	51.6	5.7	32429	22	AAH17155	Human nervous syst
45	51.4	5.7	7728	24	ABL32076	Human immune syste

## ALIGNMENTS

RESULT 1	
AA229415	
ID	AA229415 standard; cDNA; 904 BP.
XX	
AC	AA229415;
XX	
DT	29-FEB-2000 (first entry)
XX	
DE	Arabidopsis thaliana CDK inhibitor, ICK1 encoding cDNA.
XX	
KW	Cyclin-dependent kinase inhibitor; CDK; Interactor of Cdc2 Kinase 1;
KW	ICK1; Cdc2; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;
KW	antisense construct; tissue-specific promoter; transgenic plant;
KW	male sterility; ds.
XX	
OS	Arabidopsis thaliana.
XX	
Key	Location/Qualifiers
FT	55..630
FT	CDS
FT	/*tag= a
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FT	replace (318, G)
FT	/*tag= b
FT	/note= "Present in genomic DNA"
FT	40..42
FT	/*tag= c
FT	/note= "In-frame stop codon"
FT	661..663
FT	/*tag= d
FT	/note= "In-frame stop codon"
XX	
PN	W09964599-A1.

XX 16-DEC-1999.  
 XX 08-JUN-1999; 99MO-CA00532.  
 XX 08-JUN-1998; 98CA-2235978.  
 PR 31-DEC-1998; 98CA-2256121.  
 XX (MIAC) AGRIC & AGRI FOOD CANADA.  
 PA (UYSA-) UNITV SASKATCHEWAN TECHNOLOGIES INC.  
 PA (CANADA) NAT RES COUNCIL CANADA.  
 PI Wang H, Fowke LC, Crosby WL;  
 DR WPI: 2000-097540/08.  
 DR P-PSDB: AAY44335.  
 XX  
 PT Modifying plant cell development using nucleic acid encoding inhibitor  
 PT of cyclin-dependent kinase, or corresponding antisense sequence, e.g.  
 PT for inducing male sterility.  
 XX  
 PS Claim 5; Fig 1; 58pp; English.

CC The present sequence is a cDNA encoding A. thaliana Cyclin-Dependent  
 CC kinase (CDK) inhibitor, ICK1, Interactor of Cdc2 kinase 1 (ICK1)  
 CC interacts with Cdc2a, D-class cyclins, Cycd1, Cycd2 and Cycd3. Growth,  
 CC morphogenesis, multiplication, enlargement, differentiation and  
 CC maturation of plant cells can be modified by transforming them with  
 CC nucleic acid encoding CDK inhibitor or antisense construct complementary  
 CC to the inhibitor gene, operably linked to a tissue-specific promoter.  
 CC The transgenic plants exhibit alteration of traits such as petals, male  
 CC sterility and ability to set seeds.

SQ Sequence 904 BP; 307 A; 107 C; 229 G; 261 T; 0 other;

Query Match 99.6%; Score 900.8; DB 21; Length 904;  
 Best Local Similarity 99.8%; Pred. No. 3.2e-188;  
 Matches 902; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atctctctctcaagagatgttaacttcacgcacacgtaacttaattcgaagatggtg 60  
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 DB 1 atctctctctccacagagatgttaacttcacgcacacgtaacttaattcgaagatggtg 60  
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 QY 61 aagaataatagaagaagcctaaaggaattgtaagaactggaatttcgtcaacgtatcgag 120  
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 DB 61 aagaataatagaagaagcctaaaggaattgtaagaactggaatttcgtcaacgtatcgag 120  
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 QY 121 ctacggagccggaggaattggtttatgtagatcggaaataatcaagctgtctccgctgctc 180  
 |||||||  
 DB 121 ctacggagccggaggaattggtttatgtagatcggaaataatcaagctgtctccgctgctc 180  
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 QY 181 ggtgtaattgaggttcgtctgtgtatgtagaagcaatgaattaaagaagaatta 240  
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 DB 181 ggtgtaattgaggttcgtctgtgtatgtagaagcaatgaattaaagaagaatta 240  
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 QY 241 atacatctggaggaaggaataaagaatggtgaactgaactgaacttcgaacgggtg 300  
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 DB 241 atacatctggaggaaggaataaagaatggtgaactgaactgaacttcgaacgggtg 300  
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 QY 301 acggaaggaagaccttttgaataatctgagagaggaaggaagaagaattaaatcaatcc 360  
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 DB 301 acggaaggaagaccttttgaataatctgagagaggaaggaagaagaattaaatcaatcc 360  
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 QY 361 atggaataattatcatcggaatttgaatcggcggtttaaagaatcgtagattggttctgt 420  
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 DB 361 atggaataattatcatcggaatttgaatcggcggtttaaagaatcgtagattggttctgt 420  
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 QY 421 agcggaggaagaaacagatggagagcggtgaacggcgagggagggaggaagcgaaattg 480  
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 DB 421 agcggaggaagaaacagatggagagcggtgaacggcgagggagggaggaagcgaaattg 480  
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 QY 481 atgacgagagatgcacaacggaatcggaaattgaaagattttttgtggaagctgagaacaa 540

DB 481 atgacgagagatgcacaacggaatcggaaattgaaagattttttgtggaagctgagaacaa 540  
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 DB 541 ctcaagaataaattcaagaagaagtagtaacttcgatttcgagaagaagcattagaa 600  
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 QY 601 ggaactgaacatgggttaaaagttagagtgaaagaagaagaagttatggtttttt 660  
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 DB 601 ggaactgaacatgggttaaaagttagagtgaaagaagaagaagttatggtttttt 660  
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 DB 781 ctcttaacgattttagagcccaagaagtcgtgtcttttagccttactttactctt 840  
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 QY 841 ctctgaatctgtgtatcttttagcatattctttagtaattttatggtttgtgact 900  
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 DB 841 ctctgaatctgtgtatcttttagcatattctttagtaattttatggtttgtgact 900  
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 QY 901 gata 904  
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 DB 901 gata 904

## RESULT 2

ID AAC47352 standard; DNA: 779 BP.

AC AAC47352;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 53499.

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132467.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135623.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
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Query Match 85.7%; Score 774.8; DB 21; Length 779;  
Best Local Similarity 99.7%; Pred. No. 1.3e-160;

Matches 776; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 actcagcacacgtaacccaatacgaagaatggtgaagaataatagaagaagcctaaagaa 85  
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QY 86 ttgtagaagcgtgaggttcgtcaacgtatctgacgtacggaacgaggaatgtttatg 145  
DB 62 ttgtagaagcgtgaggttcgtcaacgtatctgacgtacggaacgaggaatgtttatg 121  
QY 146 ttgaatcggaaaatacgaactctgtctcgtcgtcgtgaatacgtgaatcgtcgtcct 205  
DB 122 ttgaatcggaaaatacgaactctgtctcgtcgtcgtgaatacgtgaatcgtcgtcct 181  
QY 206 gtaatggaagaatacgaataataagaagaagaataataacatctcggaggaggagaataag 265  
DB 182 gtaatggaagaatacgaataataagaagaagaataataacatctcggaggaggagaataag 241  
QY 266 atggtgacacgtaaacgtcgcgtatcgcaggggtgacgaagaagaagccttttgaataac 325  
DB 242 atggtgacacgtaaacgtcgcgtatcgcaggggtgacgaagaagaagccttttgaataac 301  
QY 326 tgaagaagaggaagaagaagaagaataatgaataacatctgagaatcttcaatcggaattg 385  
DB 302 tgaagaagaggaagaagaagaagaataatgaataacatctgagaatcttcaatcggaattg 361  
QY 386 aatcgcgaggttaagaagaatcgttgaatctgttctgaacgaggaagaagaacatcgagaga 445  
DB 362 aatcgcgaggttaagaagaatcgttgaatctgttctgaacgaggaagaagaacatcgagaga 421  
QY 446 cgtgtgacgaggaagaagaagaagaagcgaataatgatgacgagatgccaacggaatcgg 505  
DB 422 cgtgtgacgaggaagaagaagaagaagcgaataatgatgacgagatgccaacggaatcgg 481  
QY 506 aatggaagatcttttctgtgaagctgagaacaacacccaagaagaataatcaagaagaat 565  
DB 482 aatggaagatcttttctgtgaagctgagaacaacacccaagaagaataatcaagaagaat 541  
QY 566 acaattcgaattcgaagaagaagaagaagccatlaagaagacgttlaagatgggtaagctag 625  
DB 542 acaattcgaattcgaagaagaagaagaagccatlaagaagacgttlaagatgggtaagctag 601  
QY 626 agtgaagaagaagaagaagaagtttaaggttttttttaacttttaatttaatttaattta 685  
DB 602 agtgaagaagaagaagaagaagtttaaggttttttttaacttttaatttaatttaattta 661  
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QY 746 ttgaagaatcgaagaatctgacggaagaagaagaagccttttaacagattttagagccc 803  
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RESULT 3  
AAC36958  
ID AAC36958 standard; DNA; 780 BP.  
XX  
AC AAC36958;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15673.  
XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KM protein identification; signal transduction pathway;  
KM metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
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Query Match	Best Local Similarity	Matches 773: Conservative	Score 757.8: DB 21: Length 780:
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Db 1 gtgaatttcacgcaactaaccttaactgcaagaatggtgagaaatatagaaagctaaag 60			
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OY 203 ctgtatgtgaagcaatcgtatataagaagaagaatttaacacccctggaaggaagata 262
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Db 181 ctgtatgtggaagcaatcgtatataagaagaagaatttaacacccctggaaggaagata 240
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OY 323 atctgagagagagagagagagagagagagagagagagagagagagagagagagagagag 382
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OY 383 ttgaatcggcggttaaaagacgttagatctgtgttctgtagcgggagagaaacgatgagag 442
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OY 503 cggaaatcgaagatcttttctggaagctgagaacaactcaagaagaaatcgaagaaga 562
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OY 623 tagagtgagaagaagaagaagcttaagcttttctttaaactttttaaactttttaaact 682
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OY 803 c 803
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Db 780 c 780

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RESULT 4  
AA229420  
ID AA229420 standard; CDNA: 804 BP.

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AC AA229420;
DT 29-FEB-2000 (first entry)
DE Chenopodium rubrum CDKII encoding cDNA.
KW Cyclin-Dependent kinase; CDK; CDKII; Cdc2a; D-class cyclin; CycD;
KW CycD2; CycD3; morphogenesis; transgenic plant; male sterility; ds.
XX Chenopodium rubrum.
OS
FH Key Location/Qualifiers
FT CDS 58..648
FT /tag=a
FT /product="CDKII"
XX
XX WO964599-A1.
XX 16-DEC-1999.
XX
XX 08-JUN-1999; 99WO-CA00532.
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XX 08-JUN-1998; 98CA-2235978.
XX
XX 31-DEC-1998; 98CA-2256121.

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XX (MIA) AGRIC & AGRIFOOD CANADA.
PA (U.S.A.) UNIV SASKATCHEWAN TECHNOLOGIES INC.
PA (CAN) NAT RES COUNCIL CANADA.
XX Wang H, Fowke LC, Crosby WL;
PI WPI: 2000-097540/08.
DR P-PSDS; AAY44340.
XX
XX Modifying plant cell development using nucleic acid encoding inhibitor
PT of cyclin-dependent kinase, or corresponding antisense sequence, e.g.
PT for inducing male sterility.
XX Disclosure: Fig 6: 58pp; English.
XX
XX The present sequence is a cDNA encoding C. rubrum CDKII, which
CC inhibits Arabidopsis thaliana Cyclin-Dependent Kinase (CDK). CDKII
CC interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and
CC shares functional and sequence similarity with ICK1. Growth,
CC morphogenesis, multiplication, enlargement, differentiation and
CC maturation of plant cells can be modified by transforming them with
CC Agrobacterium strain harbouring an expression construct of CDKII.
CC The transgenic plants exhibit alteration of traits such as petals, male
CC sterility and ability to set seeds.
XX
XX Sequence 804 BP; 254 A; 151 C; 202 G; 197 T; 0 other;
SO

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Query Match 8.0%; Score 72.4; DB 21; Length 804;  
Best Local Similarity 62.9%; Pred. No. 1.3e-06;  
Matches 112; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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Db 477 ggcagcgaatacgaacggtacagacgaagatgcgctcgtatcgaatacgaagaaatcct 536
OY 522 tctgaagctgaagaacaactcaagaagaaatcgaagaagagagagagagagagagagagag 581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 tgcgtctgtaaaagagctccagaaagcgttcgaagagagagagagagagagagagagagag 596
OY 582 gaagagaagccattgaagagcgttacgaatgggttaagttgaagtagaagaagaaga 639
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Db 597 taaggacgtgcacatgaagagtcgtatgattggttcacataatccatgaataaa 654

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RESULT 5  
AAN02403  
ID AAN02403 standard; DNA: 470 BP.

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AC AAN02403;
DT 01-NOV-2001 (first entry)
DE Cyclin dependent kinase inhibitor (CDK1) clone s12.pX0117.h4.
KW Cyclin dependent kinase inhibitor; CDK1; herbicide; cell cycle;
KW soybean; plant growth inhibitor; ds.
XX Glycine max.
OS
FH Key Location/Qualifiers
FT CDS 2..184
FT /tag=a
FT /product="CDK1 fragment"
FT /partial
FT /note="No start codon given"
XX
XX WO20060087-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US09106.

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PR 23-MAR-1999; 99US-0125788.  
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PR 29-MAR-1999; 99US-0126785.  
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PR 08-APR-1999; 99US-0128714.  
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PR 05-MAY-1999; 99US-0132485.  
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0161947.

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Best Local Similarity 61.7%; Pred. No. 0.00011;
Matches 119; Conservative 0; Mismatches 72; Indels 2; Gaps 1;

QY 493 ccaacgaatcggaattgaatttttttggagctggaagcaacacaaagaaga 552
DB 377 ccaacacaccgcgaatgagcagatttctcgggtgctggaagcaacagaagca 436
QY 553 ttcaagaagaatgacatttcgatttcgagaagaagcattagaagacgtttacga 612
DB 437 ttcaattgagaagtaacacttgcctcgtggaacgaacacacacacgaggttga 496
QY 613 tgggttaagttaga--gttaagaagaagaagtttattgttttttttaactttta 670
DB 497 tggacgaagtgatgatttagaacaacaaaaaatgggggttaattatgataacaga 556
QY 671 gatttaatttt 683
DB 557 tatattacattt 569

RESULT 8
ID AAN02401 standard; DNA; 620 BP.
XX
AC AAN02401;
XX
DT 01-NOV-2001 (first entry)
XX
DE Cyclin dependent kinase inhibitor (CDKI) clone s12.pK0008.d2.f1s.
XX
KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle;
XX
KW soybean; plant growth inhibitor; ds.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FH CDS 1..264 /tag- a
FT /product- "CDKI fragment"
FT /partial

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FT /note= "No start codon given"
XX
XX WO2000060987-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US09106.
XX
XX 07-APR-1999; 99US-0128192.
XX
XX (DDBP) DU PONT DE NEMOURS & CO E I.
XX
XX Klein TM, Weng Z, Cahoon RE.
XX
XX WPI; 2000-679375/66.
XX
XX P-PSDB; AAP01951.
XX
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX herbicides and plant growth inhibitors
XX
XX Claim 2: Page 49; 58pp; English.
XX
XX The invention describes a novel isolated polynucleotide comprising a
XX nucleotide sequence encoding one of 17 specific cyclin dependent kinase
XX inhibitor (CDKI) polypeptides, cell cycle regulators involved in
XX control of cell division, growth and death. The nucleotide sequences can
XX be used in a vector to transform a host cell to produce the CDKI
XX polypeptide. They can also be used in methods for selecting and
XX obtaining a nucleic acid sequence that encodes CDKI or affects the level
XX of CDKI expression. The encoded protein can be used in a method for
XX evaluating a compound for its ability to inhibit the activity of a CDKI.
XX The inhibitors can be used as herbicides. They can also be used to
XX inhibit plant growth. The polynucleotide sequences can be used in gene
XX mapping and as genetic markers. The sequence encodes the soybean CDKI
XX clone s12.pK0008.d2.f1s as described in the method of the invention.
XX
XX Sequence 620 BP; 191 A; 111 C; 134 G; 183 T; 1 other:

Query Match 7.0%; Score 63; DB 21; Length 620;
Best Local Similarity 64.1%; Pred. No. 0.00014;
Matches 93; Conservative 1; Mismatches 51; Indels 0; Gaps 0;

QY 490 atgcaacgaatcggaattgaatttttttggagctggaagcaacacaaagaaga 549
DB 121 atgctaccgagttggagctgcggaatttctcgttgcgtgggaaggaacattcaga 160
QY 550 aaattcaagaagaatgacatttcgatttcgagaagaagcattagaagacgtttac 609
DB 181 cgatttcaagacaagtaacattatgttttaagagacgtacacactggaaggrcgtac 240
QY 610 gaatgggttaagttagatgaaga 634
DB 241 gagtgggttcagttgaagccatgaa 265

RESULT 9
ID AAA95287
XX
AC AAA95287;
XX
DT 17-JAN-2001 (first entry)
XX
DE Soybean cyclin-dependent kinase inhibitor coding sequence #2.
XX
KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
XX CDKI; cell growth; herbicide; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FH CDS 1..264

```



XX antiarteriosclerotic; antianemic; cytosstatic; nootropic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antineumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KW gene; ds.  
 XX Homo sapiens.  
 XX NO200200928-A2.  
 XX 03-JAN-2002.  
 XX 02-JUL-2001; 2001MO-EP07537.  
 XX 30-JUN-2000; 2000DE-1032529.  
 XX 01-SEP-2000; 2000DE-1043826.  
 XX (EPIC-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI: 2002-130909/17.  
 XX Nucleic acid comprising fragment of chemically modified gene, useful  
 PT for diagnosis and treatment of diseases associated with abnormal  
 PT cytosine methylation  
 PS Claim 1; SEQ ID NO 1294; 32pp + Sequence Listing; German.  
 XX The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.  
 XX Sequence 16509 BP; 4031 A; 379 C; 3836 G; 8263 T; 0 other;

Query Match 6.7%; Score 60.6; DB 24; Length 16509;  
 Best Local Similarity 54.8%; Pred. No. 0.0012;  
 Matches 120; Conservative 0; Mismatches 99; Indels 0; Gaps 0;  
 QY 685 agggataagttatttctgtgattggaataataagattgtaggaagattgt 744  
 DB 15468 agggtaattttattttatttattgattggaattgaggttttataaggaaagtcg 15547  
 QY 745 tttaagagtaacatgcacagaagaagaagcttttaacagatttagagccca 804  
 DB 15548 atcgttttagttcataagggagtaagagagattggaattggaggtttattata 15607  
 QY 805 gaaaagtcgtgctttagctctactcttaccctctcttcgaactctgttaccctttag 864  
 DB 15608 ttggaatttttttttttaattgattgattttaaatttagcgctttattttg 15667  
 QY 865 catattcttagtacctatttattgttttgtagctgat 903  
 DB 15668 tttatttttagtacctattttagttagttagt 15706

RESULT 12  
 AAA95293  
 ID AAA95293 standard; CDNA; 870 BP.  
 XX  
 AC AAA95293;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Arabidopsis thaliana cyclin-dependent kinase inhibitor coding sequence.

XX Cyclin-dependent kinase inhibitor; cell cycle; cell division;  
 KW CDKI; cell growth; herbicide; ss.  
 KW Arabidopsis thaliana.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..870  
 FT /\*tag= a  
 FT /product= "CDKI"  
 XX  
 XX NO200060087-A2.  
 XX 12-OCT-2000.  
 XX 06-APR-2000; 2000MO-US09106.  
 XX 07-APR-1999; 99US-0128192.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E. I.  
 XX Klein TM, Weng Z, Cahoon RE;  
 XX WPI: 2000-679375/66.  
 XX P-PSDB: AAB27262.  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors  
 PS Disclosure; Page 56-57; 58pp; English.  
 XX The present sequence is the coding sequence for the Arabidopsis thaliana  
 CC cyclin-dependent kinase inhibitor (CDKI). It was used in the isolation of  
 CC sequences from wheat, corn, rice and soybean encoding the CDKI protein.  
 CC CDKI is involved in the cell cycle, and may promote or inhibit cell  
 CC division and growth. The coding sequence and the protein it encodes are  
 CC useful in the production of transgenic plants which produce increased or  
 CC decreased amounts of the CDKI protein, in the identification of  
 CC herbicides, in genetic and physical mapping and in the isolation of the  
 CC CDKI gene in other organisms.  
 XX Sequence 870 BP; 265 A; 185 C; 203 G; 217 T; 0 other;

Query Match 6.7%; Score 60.4; DB 21; Length 870;  
 Best Local Similarity 65.7%; Pred. No. 0.00056;  
 Matches 88; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
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 QY 553 ttcaagaagaatgcaatttcgatttcgaagaagaaagcattagaagagcttagcga 612  
 DB 790 ttcatltaggaagtagcaactttgtatcctgtgaacaacaactaccagagcgtttgaa 849  
 QY 613 tgggtaaagttaga 626  
 DB 850 tggacgaaggtaga 863

RESULT 13  
 AAC46465  
 ID AAC46465 standard; DNA; 870 BP.  
 XX  
 AC AAC46465;  
 XX  
 DT 18-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 50239.  
 XX  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway;

metabolic pathway; promoter; termination sequence; ss.  
Arabidopsis thaliana.  
EP1033405-A2.  
06-SEP-2000.  
25-FEB-2000; 2000EP-0301439.  
99US-0121825.  
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PR 29-OCT-1999; 99US-0162142.

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Query Match      6.7%; Score 60.4; DB 21; Length 870;
Best Local Similarity 65.7%; Pred. No. 0.00056;
Matches 86; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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QY 553 ttcagaagaagatcacatttcgatttcgagaagaagaaacacattgaagagcttaagaa 612
    ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
DB 790 ttctatgaagaagtacactttgacctccttgatcgacgaacacacactacagagctttgaa 849
QY 613 tgggtaaagttaga 626
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DB 850 tggacgaaggtaga 863

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RESULT 14
AAK25038
ID AAK25038 standard; DNA: 69 BP.
XX
AC AAK25038;
XX
DT 05-JUL-1999 (first entry)
XX
DE Cyclin-dependent kinase inhibitor LDV159 cDNA PCR primer.
XX
KW Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI;

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KW LDV159; CKI; plant development; transgenic plant; cell cycle;
KW growth regulator; herbicide; PCR; primer; ss.
OS Synthetic.
OS Arabidopsis thaliana.
PN W09914331-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98MO-EP05895.
XX
PR 24-DEC-1997; 97EP-0204111.
PR 16-SEP-1997; 97EP-0202838.
XX
PA (CROP-) CROPEDESIGN NV.
XX
PI De Almeida J, De Veylder L, Inze D, Landrieu I;
XX
DR WPI; 1999-229535/19.
XX
PT DNA encoding inhibitor of cyclin-dependent kinase
XX
PS Example 10; Page 56; 88pp; English.
XX
CC The present sequence was used as a primer, together with the primer
CC given in AAK25039, for the PCR amplification of LDV159 cDNA coding
CC region. LDV159 is a cyclin-dependent kinase (CDK) inhibitor of
CC Arabidopsis thaliana, and is identical to previously known CKI.
CC The PCR fragment was cloned into vector pTA7002. The resulting
CC binary vector was transferred into Agrobacterium tumefaciens and
CC used to transform tobacco cv. Petit Havana to produce transgenic
CC plants that overexpressed the CDK inhibitor. Several CDK
CC inhibitors have been shown to exist in plants. They are expressed
CC at different time points and may have different functions during
CC the development of the plant. CDK inhibitors, nucleic acids,
CC antibodies, promoter sequences, related recombinant DNA and
CC vectors are all useful for: modulating the cycle, division and/or
CC growth of plant cells; altering activity of CDK; modulating growth
CC inhibition in plants caused by environmental stress; inducing male
CC or female sterility; altering cell division progression in plants;
CC bacteria, fungi, insect and animal cells; and screening for
CC agonists or antagonists that are potentially useful as growth
CC regulators or herbicides.
XX
SQ Sequence 69 BP; 24 A; 10 C; 19 G; 16 T; 0 other;

```

```

Query Match      6.6%; Score 59.4; DB 20; Length 69;
Best Local Similarity 98.4%; Pred. No. 0.00045;
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 53 agatgtgtaaaataatagaagaagctgaaggaattagaagctgagatttcgtaacgt 112
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DB 9 agatgtgtaaaataatagaagaagctgaaggaatttcgtaagctgagatttcgtaacgt 68
QY 113 a 113
Do 69 a 69

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```

RESULT 15
ABL33226
ID ABL33226 standard; DNA: 13125 BP.
XX
AC ABL33226;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SRQ ID NO: 1199.
XX
KW Human; immune system disease; cytosine methylation; antistimatic;
antiartherosclerotic; antianaemic; cyostatic; nootropic;

```

XX neuroprotective; anti-HIV; anticoagulant; ophthalmologic;  
KW antihemematic; antiarthritic; antidiabetic; antipsoriatic;  
KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
KW gene; ds.  
XX  
XX Homo sapiens.  
OS  
PN WO200200928-A2.  
PD  
PD 03-JAN-2002.  
XX  
XX 02-JUL-2001; 2001WC-EP07537.  
PF  
XX 30-JUN-2000; 2000DE-1032529.  
PR  
FR 01-SEP-2000; 2000DE-1043826.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K:  
PI  
XX WPI: 2002-130909/17.  
DR  
XX  
XX Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PI cytosine methylation -  
PT  
XX  
XX  
PS Claim 1; SEQ ID NO 1199; 32pp + Sequence Listing; German.  
XX  
XX "The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
CC diseases. The present sequence is a gene of the invention.  
XX  
XX Sequence 13125 BP; 3546 A; 246 C; 2776 G; 6555 T; 2 other;

Query March\_1000000000 5.5%; Score 58.8; DB 24; Length 13125;  
Best Local Similarity 53.8%; Pred. No. 0.0027;  
Matches 143; Conservative 0; Mismatches 122; Indels 1; Gaps 1.

GenCore Version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 15:54:59 ; Search time 1823.05 Seconds  
(without alignments)  
10376.890 Million cell updates/sec

Title: US-09-733-507-1

Perfect score: 904  
Sequence: 1 atctctctctcacagaga.....tatgtttttgtgactgata 904

Scoring table: IDENTITY\_NUC  
Gapex 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_hg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_to:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_la:\*  
19: em\_ma:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_to:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hg\_hum:\*  
31: em\_hg\_inv:\*  
32: em\_hg\_other:\*  
33: em\_hggo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query  
No. Score Match Length DB ID Description

1	904	100.0	904	6	AX008791	AX008791 Sequence
2	851.2	94.2	856	8	AT094772	U94772 Arabidopsis
3	656.8	72.7	660	6	AX008793	AX008793 Sequence
4	544.8	60.3	1240	8	AF079587	AF079587 Arabidops
5	543.2	60.1	98374	8	AC003040	AC003040 Arabidops
6	364	40.3	443	6	AX008794	AX008794 Sequence
7	339.2	37.5	377	6	AX008795	AX008795 Sequence
8	92.6	10.2	7218	6	AB02943	AB02943 Sequence 14
9	75	8.3	927	8	AB02943	AB02943 Pisum sat
10	72.4	8.0	804	6	AX008805	AX008805 Sequence
11	72.4	8.0	804	8	CR002173	AX002173 Chenopodi
12	69.4	7.7	789	8	NT0297306	NT0297306 Nicotiana
13	69	7.6	286564	2	AC091428	AC091428 Mus muscu
14	66.8	7.4	203606	2	AL645990	AL645990 Mus muscu
15	65	7.2	223547	2	AL611963	AL611963 Mus muscu
16	64.6	7.1	223828	2	AC098731	AC098731 Mus muscu
17	64.2	7.1	231122	2	AC090480	AC090480 Mus muscu
18	63.8	7.1	201109	2	AL591709	AL591709 Homo sapi
19	62.8	6.9	282611	2	AL645746	AL645746 Mus muscu
20	62.6	6.9	161475	9	HS164C20	AL009029 Homo sapi
21	62.2	6.9	203994	2	AC067854	AC067854 Homo sapi
22	62	6.9	111345	2	AL445531	AL445531 Human DNA
23	62	6.9	236962	2	AL606742	AL606742 Mus muscu
24	61.8	6.8	157848	9	AC079763	AC079763 Homo sapi
25	61.6	6.8	63739	2	AC102458	AC102458 Mus muscu
26	61.6	6.8	75241	2	AC102370	AC102370 Mus muscu
27	61.6	6.8	179149	9	AC009785	AC009785 Homo sapi
28	61.6	6.8	205638	2	AC040927	AC040927 Mus muscu
29	61.6	6.8	252937	2	AC105705	AC105705 Rattus no
30	61.4	6.8	153588	9	AC010533	AC010533 Homo sapi
31	61.4	6.8	175562	2	AP002833	AP002833 Homo sapi
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34	61.4	6.8	224712	2	AL606969	AL606969 Mus muscu
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37	61	6.7	165077	10	AC084382	AC084382 Mus muscu
38	60.8	6.7	201395	10	AC091250	AC091250 Mus muscu
39	60.8	6.7	234777	2	AL670236	AL670236 Mus muscu
40	60.5	6.7	16509	6	AX346223	AX346223 Sequence
41	60.6	6.7	71910	2	AC102027	AC102027 Mus muscu
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44	60.2	6.7	173732	2	AC099625	AC099625 Mus muscu
45	60.2	6.7	205751	2	AL645611	AL645611 Mus muscu

## ALIGNMENTS

RESULT 1  
LOCUS AX008791 904 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 1 from Patent WO9964599.  
ACCESSION AX008791  
VERSION AX008791.1 GI:9996255  
KEYWORDS

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 904)  
Fowke, L.C., Wang, H. and Crosby, W.L.  
Cyclin-dependent kinase inhibitors as plant growth regulators  
Patent: WO 9964599-A 1 16-DEC-1999;  
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD  
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV  
SASKATCHEWAN TECHNOLOGIES (CA)

## FEATURES

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/organism="Arabidopsis thaliana"  
/db\_xref="taxon:3702"



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KOLTEKFNKTIKFDPEKPLEGIVEVKLE"
BASE COUNT
307 a 107 c 229 g 261 t
ORIGIN

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Query Match	100.0%;	Score 904;	DB 6;	Length 904;
Best Local Similarity	100.0%;	Pred. NO. 3e-170;		
Matches 904;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

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QY	61	agaaatatagaagaagcttaaggaattgtgaagctggagtttcgtcaagctatgcaag	120
Db	61	AGAAATATATAGAAAGCTATAGGAATGTATGAAGCTGGAGTTTCTGTCACCTATATGACAG	120
QY	121	ctaaggagccggagaattgtttatgttaatctggaaaaataaagtcgtctcgtctgc	180
Db	121	CTACGGACCCGGAATGTTTATGTTAATGGAAAAATCAAGCTGTCTCGTCTGTC	180
QY	181	ggtgataatgagcttcgtctcgtctgttagtggaagcaatgaataaagaagaagta	240
Db	181	GGTGATTAATGAGATTTCGTCTCTGTATGTGCAAGCAATATATAAATAAAGATTA	240
QY	241	atacatctgsgsgsgaagaataaagatggtgacatgaaacgtcgagctatcgacgggctg	300
Db	241	ATACATCTCGSAGSGAGAAAGATTAAGATGTGGACACTGAAACCTCGACTACGACGGGTG	300
QY	301	acgaagagaagagcttttggaaatctggaagagaagagaagaagaagaaatgaatnacc	360
Db	301	ACGAAGAGAGAGCTTTTGGAAATCTGAGAGAGAGAGAGAGAAAGAAATTAAGTAAATCC	360
QY	361	atggagaattatcatctcgaaattggaatcggcggttaagaaatcgtltgaattgctgtgt	420
Db	361	ATGGAGAAATATCATCTCGAATTGGAATCGCGCGGTAAAGATCGTTAGATTGTGTGT	420
QY	421	agcgggagagaacagatggaagagagacggtgacggcgagagagaagagaagcggaattg	480
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QY	481	atcgacggagatgcccacagcgaaatcgaaattggaatttttcgtggaagctgaagaaca	540
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QY	781	ctttttaacagattttaagcccaagaagaatcgctgtcttttagcttaacttaccctt	840
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RESULT	2	
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DEFINITION	Arabidopsis thaliana cyclin-dependent kinase inhibitor protein (ICK1) mRNA, complete cds.	
ACCESSION	U94772	
VERSION	U94772.1	GI:2052501
KEYWORDS		
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	

REFERENCE	1 (bases 1 to 856)
AUTHORS	Wang, H., Fowke, L.C. and Crosby, W.L.
TITLE	A plant cyclin-dependent kinase inhibitor gene
JOURNAL	Nature 386 (6624), 451-452 (1997)
MEDLINE	97242401
REFERENCE	2 (bases 1 to 856)
AUTHORS	Wang, H., Fowke, L.C. and Crosby, W.L.
TITLE	Direct Submission
JOURNAL	Submitted (20-MAR-1997) Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada
FEATURES	Location/Qualifiers

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gene        1. .856
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CDS         7. .582

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Best Local Similarity	99.6%	Pred. No. 9,7e-160		
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Qy	109	acgtatctgagctacgagccgcggaattcttatcttgaatcgcgnaaaatccaagctct	168
Db	61	ACGTATCTGAGCTACGAGCCGCGGAATTTTATGTTTATGATCGSAAAAATCAAGGCT	120
Qy	169	gtctccgctgctgagatataatgagttctcgctcttctgaatgagaaatgaaataaag	228
Db	121	GTCCTCCGCTGCTGGTATATGAAATTCGTCGCTTGATGTAAGCAATTAATATAG	180
Qy	229	aagaagaataatactatctctgagagaggaataaataatgtgatacttaaacgttcagc	288
Db	181	AAGAAGAATTAATACATCTGGAGSAGGAGATTAAGATGTGTACCTTAACGTCGAGC	240

QY 289 tatcgacgggtgacgaagaagaaagcttttggaaaatctggagaagaggaagaagaaga 348  
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 Db 241 TATCGACGGGGTACGAAAGAGAGCTTTGTAATAATCTGAGAGGAGGAGAAAGAGAA 300  
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 Db 301 TTAAGTAATCCATGAGAAATATTATTCATCGGAATTTGAATGGCGGTTAAGAAATCGTTA 360  
 QY 409 gattgttcttgaacgaggaagaagaacgattgagagacggtgacgcgaggaaggaag 468  
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 Db 361 GATTGTGTTGTAGCGGAGGAGAAACGATGAGAGAGACGGTGACGGCGGAGAGAGAGAG 420  
 QY 469 aagggcaaatgatgacgagagatgccacggaatcggaatcttggaaatcttctgtgaa 528  
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 Db 421 AAGCGGAATTCATGACGAGATGCCACAGGAATCGGAATTTGAAGATTTTGTGGAA 480  
 QY 529 gctgagaaacaaactaaagaagaatcaagaagaatcaaatctgcattcgcgaagaag 588  
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 Db 601 TGGTTTTTTTTTAACCTTTTATGATTTAATTTCAAGGAAATTAATTTATTTTATTTG 660  
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 ACCESSION AX008793  
 VERSION AX008793.1 GI:9996257  
 KEYWORDS  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 660)  
 REFERENCE Fowke L.C., Wang H. and Crosby W.L.  
 AUTHORS Cyclin-dependent kinase inhibitors as plant growth regulators  
 JOURNAL Patent: WO 9964599-A 3 16-DEC-1999;  
 FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD  
 (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV  
 SASKATCHEWAN TECHNOLOGIES (CA)  
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 QY 169 gtctccctcgtcgtgataatggaattcgtcgtctgtatgttgaagaatgataaag 228  
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 Db 361 AAGCGGAATTCATGACGAGATGCCACAGGAATCGGAATTTGAAGATTTTGTGGAA 420  
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 Db 421 GGTGAGAAACAACTCAAGAAATAATCAAGAGAGATCAATTTTCGATTCGAGAAAGAG 480  
 QY 589 aagccattagaagacgttacgaatcggtlaaagttagagtgaaagaagaagaagctta 648  
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 Db 481 AAGCCATTGAGAGAGAGCTTACGAATGGGTAAAGTTAGAGTAAAGAGAGAGAGCTTA 540  
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 AF079587 1240 bp DNA linear PLN 07-SEP-1998  
 LOCUS AF079587  
 DEFINITION Arabidopsis thaliana cyclin-dependent kinase inhibitor (ICK1) gene,  
 complete cds.  
 ACCESSION AF079587  
 VERSION AF079587.1 GI:3550261  
 KEYWORDS  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 1240)  
 REFERENCE Wang H., Qi Q., Schorr P., Cutler A.J., Crosby W.L. and Fowke L.C.  
 AUTHORS ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis  
 JOURNAL thaliana interacts with both Cdc2a and CycD3, and its expression is  
 MEDLINE induced by abscisic acid  
 98426383 Plant J. 15 (4), 501-510 (1998)  
 2 (bases 1 to 1240)  
 REFERENCE Wang H.  
 AUTHORS Direct Submission  
 JOURNAL Submitted (21-JUL-1998) Saskatoon Research Centre, Agriculture and  
 Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada

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ORGANISM Arabidopsis thaliana
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 98374)
REFERENCE
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnes S.E., Bartsch M.E.,
Feldblum J.V., Bell C.R., Ketchum K.A., Lee J.J., Konning C.M.,
Koo H., Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Mayan L.,
Tallon B.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Niernan W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M. and
Venter J.C.
Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana
Nature 402 (6763), 761-768 (1999)
JOURNAL MEDLINE 20083487
PUBMED 10617197
REFERENCE 2 (bases 1 to 98374)
AUTHORS Lin X.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
COMMENT On Dec 17, 1999 this sequence version replaced gi:3242700.

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The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (<http://www.tigr.org/cdb/at.html>).

Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (<http://arthur.epm.ornl.gov/pub/graill/>), GeneFinder (Phil Green, University of Washington), GenScan (Chris Burge, <http://genome.stanford.edu/GENSCAN.html>), and NetPlantGene (<http://www.cbs.dtu.dk/services/NetGene2/>), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats were identified by RepeatMasker (Arian Smil, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/Masnu/ABI consortium for sequencing BAC clones F6p23, F5b6, T17A5, and T13116, the ESSA group for sequencing clone F11D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Likin Zhou, Hanif Khajak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

Address all correspondence to: [atetigr.org](mailto:atetigr.org).

## FEATURES

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Location/Qualifiers

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REFERENCE	AUTHORS	TITLE
(bases 1 to 443)	Fowke, L.C., Wang, H. and Crosby, W. L.	Cyclin-dependent kinase inhibitors as plant growth regulators
	Patent: WO 96/459-A 4, 16-DEC-1995	
	FOUR LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRI-FOOD CANAL	
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	SASKATCHEWAN TECHNOLOGIES (CA)	

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BASE COUNT	138 a 31 c 109 g 99 t
ORIGIN	

Query Match:	37.5%;	Score 39.2;	DB 6;	Length 377;
Best Local Similarity	94.1%;	Pred. No. 8.4e-58;		
Matches 369;	Conservative 0;	Mismatches 8;	Indels 15;	Gaps 1
QY	285	gaactatcgacgggtgacgaagagaaagctttttaaatactcgagagagggaggaaga	344	
DB	1	GAGTATTTTAAAGGGGTGACGAGAGCAAGCTTTTGAATCGATCGAAGACGAGCAAGA	60	
QY	345	agaattaaagaaatccatgagaaatattcatcgaaattttaaactcggggtttaaagatc	404	
DB	61	AGATTAAAGTAAACCTATGAGAGAAATTATTCATCGAATTTGAATCGCGGTAAAGAAATC	120	
QY	405	gttagatattgttgt	464	
DB	121	GTTGAAATGT	165	
QY	465	ggaagaaggcgaatltgatgcggaagatgccaaacggaatcggaaattgaagattttttgt	524	
DB	166	GAGGAAGCGGAATTTGATGACGAGAGATGCCAACGGAATCGGAAATTGTAAGATTTTTGT	225	

Oy	525	ggagcgcgagaaacaaactcaaaagaaaatctcaagagacagatcaacttcgattcgaga	584
Db	226	GGAGGCTGGAATAACAACCTCAAGAAAAAATTCAGAGAGAGATCAATTTGATTTGGA	285
Oy	585	ggaacagccactagaagagacgtctacgaatcggtaagcttagagtgaaagaaagaaag	644
Db	286	GGAAACCCCTTTGAAGAGACCTTACCAATAGGCTTAAGTTAAGTCAAGAAAGAACAA	345
Oy	645	ttatcgctttctttttaactttttagatctt	676
Db	346	TTTATGGTTTTTTTTTAACTTTTAGATTTT	377

RESULT	8				
LOCUS	166494/c				
DEFINITION	Sequence 14 from patent US 5670367.	7218 bp	DNA	linear	PAT 28-DEC-1997
ACCESSION	166494				
VERSION	166494.1	GI:2724471			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified				
AUTHORS	1 (bases 1 to 7218)				
TITLE	Dörner, F., Scheiflinger, F. and Falkner, F. Ginter.				
JOURNAL	Recombinant fowlpox virus				
FEATURES	Patent: US 5670367-A 14 23-SEP-1997;				
SOURCE	Location/Qualifiers				
	1..7218				
	/organism="unknown"				
BASE COUNT	1944 a	1491 c	1486 g	1929 t	366 others
ORIGIN					

Query Match	10.2%	Score 92.6	DB 6	Length 7218
Best Local Similarity	4.9%	Prod. No. 1.1e-08		
Matches 20	Conservative	255	Mismatches 134	Indels 0
				Gaps 0
QY 237	attaatacatctggaaggaggaagataaagatggtacacatgaaacgttcgacgtatcgacg	296		
DB 1473	ATCATGCAAGTAAGTAAAGATAGAGAATTTGGTACRRRRRRRRRRRRRRRRRRRR	1414		
QY 257	ggtgacgaaggaggaagcgtttttaaatactggagaggaaggagaagaagattaa	356		
DB 1413	RR	1354		
QY 357	atccatggaagatattatcatcggaatttgaatcgcggttaagaatcgttagtttg	416		
DB 1355	RR	1294		
QY 417	ttgtgcgggaggaagaacgattggaagaacggtgaacgcggaggaaggaggaagcgaa	476		
DB 1293	RR	1234		
QY 477	attgtagcgaagrtgtgccaacggaatcoggaatttgaagatttttltgysaagctgaa	536		
DB 1233	RR	1174		
QY 537	acaactcaagaanaaattccaagaagaatcaattcgatttcgagaaggaggaagccatt	596		
DB 1173	RR	1114		
QY 597	aaaagaagcgttagcgaatcggttaagttgaagttgaagaagaagaagaagt	645		
DB 1113	RRRT	1065		

RESULT 9

AB029483

LOCUS

DEFINITION Pisum sativum ckl mRNA for cyclin dependent kinase inhibitor, complete cds.

927 bp

mRNA

linear

PLN 11-JAN-2000





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/db_xref="GI:2653281"
/translation="MAAATPTSSPAKKIKKVKSSYNIPOLRSRKNLAPENFAEL
ETTPLEVAAYVEEVEVANCSSSEYITTAARDPPSCSSSYDLSSEVEYKDDDL
GNRTADPEVESEKSKOKESHRTAREARKLDQPTPKSTVQIKMPSDEIEEFF
AAVAKDLQKRESEKYNFDIVKVPKGRDWPVNP"
BASE COUNT      254 a      151 c      202 g      197 t
ORIGIN

Query Match      8.0%: Score 72.4; DB 8; Length 804;
Best Local Similarity 62.98; Pred. No. 0.00011;
Matches 112; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 462 ggaagaaagcgaatgatgacgagatgcacaggaatcggaaattgaattttt 521
    || || || || || || || || || || || || || || || || || || || ||
Db 477 GGCGAGCAATTCACGCGTACAGATCAAGATCCCGTGTATCAAGAAATCGAAGATCTT 536

QY 522 tctggaagctggaacaactccaagaataatccaagaagtagaattcgattcga 581
    || || || || || || || || || || || || || || || || || || || ||
Db 537 TCGTGTGCTGAAAAAGATCTCCAGAAAGCGCTTCAGCGAAAGTACATTTGACATAGT 596

QY 582 gaaggaagacccattagagagccttagcaatgggtlaaagttagagtcgaagaaga 639
    || || || || || || || || || || || || || || || || || || || ||
Db 597 TAAGGACGTGCCACTGAAGGTCGTATGATTGGTTCATTAATCCATGAATATAA 654

RESULT 12
LOCUS      NTO297906      789 bp      mRNA      linear      PLN 03-OCT-2001
DEFINITION Nicotiana tomentosiformis mRNA for CDK/cyclin inhibitor (Kisla
            gene).
ACCESSION  AJ297906.1 GI:15963347
VERSION     AJ297906.1
KEYWORDS    CDK/cyclin inhibitor; Kisla gene.
SOURCE      Nicotiana tomentosiformis.
ORGANISM    Nicotiana tomentosiformis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterias I; Solanales; Solanaceae; Nicotiana.
REFERENCE   1 (bases 1 to 789)
AUTHORS     Grandard,S., Perennes,C., Bernardi,F., Bergounioux,C. and Glab,N.
TITLE       The tobacco CDK inhibitor NtKisla is involved in flower development
JOURNAL     Unpublished
AUTHORS     Grandard,S.
TITLE       Direct Submission
JOURNAL     Submitted (23-Oct-2000) Grandard S., Science de la vie, CNRS,
            Universite, IBP, Universite Paris Sud, Bat 630, Orsay, 91405,
            FRANCE
FEATURES
  source          1..789
                  Location/Qualifiers
  5'UTR           1..72
                  /organism="Nicotiana tomentosiformis"
                  /db_xref="taxon:4098"
  gene           1..789
                  /gene="Kisla"
  CDS             73..564
                  /gene="Kisla"
                  /function="cell cycle regulator"
                  /codon_start=1
                  /product="CDK/cyclin inhibitor"
                  /protein_id="CAC82733.1"
                  /db_xref="GI:15963348"
                  /translation="MRKKGIEVYTIMEVDLEVPITTKRRKISSDGVKLMSPL
                  LKCRSHGVGDPAGSIVSPSSVNLNADSLDGLVLRNNGSSSENVLASASK
                  EAKLSSEKQRTPEKMPSEKIEFFFAAKAKILKRFKKKINPFEKEEPLSGRYENVR
                  IGS"
  3'UTR          565..789
                  /gene="Kisla"
  BASE COUNT     256 a      126 c      197 g      210 t
  ORIGIN

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Query Match      7.7%: Score 69.4; DB 8; Length 789;
Best Local Similarity 66.28; Pred. No. 0.00044;
Matches 100; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 486 ggaatgccaagaaatcgaatgaagatttttctggaagctggaacaactcaa 545
    || || || || || || || || || || || || || || || || || || || ||
Db 417 GAAATGCCGCTGAAAAAGAGATTGAAGATTTTTCAGCTGCCAGAAAGCTATACT 476

QY 546 agaaaaattcaagaagaagtacatttcgatttcgaaagagaagacattaaagacg 605
    || || || || || || || || || || || || || || || || || || || ||
Db 477 TAAACGATTAGAAAAAGTACAACTTCGACTTGAAGAAAGAGAGCCATTGGAAGGTGC 536

QY 606 ttacgaatgggtlaaagttagatgaagaaga 636
    || || || || || || || || || || || || || || || || || || || ||
Db 537 CTACGAATGGGTCCGCAATAGGAAGTGTAGAGA 567

RESULT 13
LOCUS      AC091428      286564 bp      DNA      linear      HTG 20-APR-2001
DEFINITION Mus musculus chromosome 11 clone : MGS1-185K22, MGS1-180K15,
            MGS1-219P9, MGS1-65111, *** SEQUENCING IN PROGRESS ***, 11
            unordered pieces.
ACCESSION  AC091428
VERSION     AC091428.1 GI:13699334
KEYWORDS    HTG; HTGS_PHASE1; HTGS_FULLTOP.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 286564)
AUTHORS     Resch,K., Platzer,M., Fuchs,S., Schlubel,M., Jockusch,H.,
            Rosenthal,A. and Schmitt-John,T.
TITLE       Chromosome 11 genomic sequence
JOURNAL     Unpublished
AUTHORS     Platzer,M.
TITLE       Direct Submission
JOURNAL     Submitted (20-APR-2001) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT     * NOTE: This is a 'working draft' sequence. It currently
            * consists of 11 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1
            * 12871: contig of 12871 bp in length
            * 12872 12971: gap of unknown length
            * 12972 62053: contig of 49082 bp in length
            * 62054 62153: gap of unknown length
            * 62154 233520: contig of 191367 bp in length
            * 233521 233620: gap of unknown length
            * 233621 258176: contig of 4556 bp in length
            * 258177 258276: gap of unknown length
            * 258277 263203: contig of 4927 bp in length
            * 263204 263303: gap of unknown length
            * 263304 267782: contig of 4479 bp in length
            * 267783 267882: gap of unknown length
            * 267883 277416: contig of 9534 bp in length
            * 277417 277516: gap of unknown length
            * 277517 279532: contig of 2016 bp in length
            * 279533 279632: gap of unknown length
            * 279633 282059: contig of 2427 bp in length
            * 282060 282159: gap of unknown length
            * 282160 284288: contig of 2129 bp in length
            * 284289 284389: gap of unknown length
            * 284390 286564: contig of 2176 bp in length.
            *
            * 1..286564
            * Location/Qualifiers

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QY 571 ttcgatttcgaggagagag 591  
| | | | | | | | | |  
Db 217989 GAGAGAGAGAGAGAGAG 217969

Search completed: September 4, 2002, 18:25:33  
Job time: 9034 sec

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